A-688A (rev 12-6-04).ST25.txt
SEQUENCE LISTING

<110>  FEIGE, ULRICH
       KOHNO, TADAHIKO
       LACEY, DAVID
       BOONE, THOMAS CHARLES

<120>  ADHESION ANTAGONISTS (as amended)

<130>  A-688A

<140>  US 09/840,277
<141>  2001-04-23

<150>  US 60/198,919
<151>  2000-04-21

<150>  US 60/201,394
<151>  2000-05-03

<160>  161

<170>  PatentIn version 3.2

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Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15


ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc        96
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                20                  25                  30


atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc       144
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
            35                  40                  45


cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag       192
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        50                  55                  60


gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg       240
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80


tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat       288
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95


ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc       336
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
                100                 105                 110


atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag       384
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            115                 120                 125


gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc       432
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Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130             135             140

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg      480
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145             150             155             160

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct      528
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            165             170             175

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc      576
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180             185             190

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg      624
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            195             200             205

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg      672
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210             215             220

tct ccg ggt aaa                                                       684
Ser Pro Gly Lys
225


<210>  2
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Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5               10              15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20              25              30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35              40              45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50              55              60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65              70              75              80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85              90              95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100             105             110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            115             120             125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
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Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

Ser Pro Gly Lys
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Gly Gly Gly Lys Gly Gly Gly Gly
1               5


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Gly Gly Gly Asn Gly Ser Gly Gly
1               5


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Gly Gly Gly Cys Gly Gly Gly Gly
1               5

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Gly Pro Asn Gly Gly
1               5


<210>  7
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Tyr Ile Gly Ser Arg
1               5


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Glu Cys Glu Ser Gly Pro Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu
1               5                   10                  15


Gly Thr Ile Cys Lys Arg Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys
            20                  25                  30


Asn Gly Lys Thr Cys Asp Cys Pro Arg Asn Pro His Lys Gly Pro Ala
            35                  40                  45


Thr


<210>  9
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<220>
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<222>  (2, 5 and)..(7)
<223>  Xaa is any amino acid
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Arg Xaa Glu Thr Xaa Trp Xaa
1               5


<210> 10

<400> 10
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<210> 11
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<220>
<221> misc_feature
<222> (2, 3, 7 and)..(8)
<223> Xaa is any amino acid

<400> 11

Cys Xaa Xaa Arg Leu Asp Xaa Xaa Cys
1               5


<210> 12

<400> 12
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<210> 13
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<213> Artificial Sequence

<220>
<223> RGD, NGR derivative peptide


<220>
<221> misc_feature
<222> (1, 2, 3, 7, 8 and)..(9)
<223> Xaa is any amino acid with Xaa at 1, 3, 7 and 9 capable of
      forming a bridge.

<400> 13

Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa
1               5


<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> RGD, NGR derivative peptide


<220>

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<221>  misc_feature
<222>  (2, 3, 4, 5, 6, 12, 13, 14, 15 and)..(16)
<223>  At positions 2, 3, 4, 5, 6, 12, 13, 14, 15 and 16, Xaa is any
       amino acid or may be absent.

<400>  14

Cys Xaa Xaa Xaa Xaa Xaa Cys Arg Gly Asp Cys Xaa Xaa Xaa Xaa Xaa
1               5                   10                  15


Cys



<210>  15
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<212>  PRT
<213>  Artificial Sequence

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<223>  RGD, NGR derivative peptide


<220>
<221>  misc_feature
<222>  (1 and)..(8)
<223>  Xaa is an independently selected amino acid.

<220>
<221>  misc_feature
<222>  (2 and)..(7)
<223>  Xaa is any amino acid, each which is independently selected.

<220>
<221>  misc_feature
<222>  (5)..(5)
<223>  Xaa is selected from the group consisting of glycine and leucine.

<220>
<221>  misc_feature
<222>  (6)..(6)
<223>  Xaa is selected from the group consisting of tryptophan and
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<400>  15

Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa
1               5


<210>  16
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<220>
<221>  misc_feature
<222>  (1 and)..(10)
<223>  Xaa is any amino acid.

<220>
<221>  misc_feature
<222>  (2 and)..(9)
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<223>  Xaa equals 0 to 3 amino acids.

<220>
<221>  misc_feature
<222>  (3)..(3)
<223>  Xaa is selected from the group consisting of tryptophan and
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<220>
<221>  misc_feature
<222>  (6)..(6)
<223>  Xaa is selected from the group consisting of glycine and leucine.

<220>
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<222>  (7)..(7)
<223>  Xaa is selected from the group consisting of tryptophan and
       leucine.

<220>
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<222>  (8)..(8)
<223>  Xaa is selected from the group consisting of leucine, tryptophan,
       and methionine.

<400>  16

Xaa Xaa Xaa Asp Asp Xaa Xaa Xaa Xaa Xaa
1               5               10


<210>  17
<211>  19
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<220>
<221>  misc_feature
<222>  (3, 5, 6, 13 )..(15)
<223>  Xaa is any naturally occuring amino acid residue.

<400>  17

Arg Lys Xaa Asn Xaa Xaa Trp Thr Trp Val Gly Thr Xaa Lys Xaa Leu
1               5               10              15


Thr Glu Glu


<210>  18
<211>  16
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<220>
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<222>  (2, 3, 4, 7 )..(15)
<223>  Xaa is any naturally occuring amino acid residue

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Cys Xaa Xaa Xaa Tyr Thr Xaa Leu Val Ala Ile Gln Asn Lys Xaa Glu
1               5                   10                  15


<210> 19
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<212> PRT
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<222> (3, 4, 5, 6, 8, 13, 15 )..(18)
<223> Xaa is any naturally occuring amino acid residue.

<400> 19

Arg Lys Xaa Xaa Xaa Xaa Trp Xaa Trp Val Gly Thr Xaa Lys Xaa Leu
1               5                   10                  15


Thr Xaa Glu


<210> 20
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<223> Xaa is any naturally occuring amino acid residue.

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Ala Xaa Asn Trp Xaa Xaa Xaa Glu Pro Asn Asn Xaa Xaa Xaa Glu Asp
1               5                   10                  15


<210> 21
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<223> Xaa is any naturally occuring amino acid residue.

<400> 21

Xaa Lys Xaa Lys Thr Xaa Glu Ala Xaa Asn Trp Xaa Xaa

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<400> 22

Cys Leu Cys Arg Gly Asp Cys Ile Cys
1               5


<210> 23
<211> 8
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<400> 23

Cys Trp Asp Asp Gly Trp Leu Cys
1               5


<210> 24
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<400> 24

Cys Trp Asp Asp Leu Trp Trp Leu Cys
1               5


<210> 25
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<400> 25

Cys Trp Asp Asp Gly Leu Met Cys
1               5


<210> 26
<211> 8
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<400> 26

Cys Trp Asp Asp Gly Trp Met Cys
1               5


<210>   27
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<400>   27

Cys Ser Trp Asp Asp Gly Trp Leu Cys
1                   5


<210>   28
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<400>   28

Cys Pro Asp Asp Leu Trp Trp Leu Cys
1                   5


<210>   29
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Asn Gly Arg
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<400>   30

Gly Ser Leu
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<210>   31
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<400> 31

Arg Gly Asp
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<210> 32
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<400> 32

Cys Gly Arg Glu Cys Pro Arg Leu Cys Gln Ser Ser Cys
1               5               10


<210> 33
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Cys Asn Gly Arg Cys Val Ser Gly Cys Ala Gly Arg Cys
1               5               10


<210> 34
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<400> 34

Cys Leu Ser Gly Ser Leu Ser Cys
1               5


<210> 35
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<400> 35

Gly Ser Leu
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<210> 36
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<400> 36

Asn Gly Arg Ala His Ala
1               5


<210> 37
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<400> 37

Cys Asn Gly Arg Cys
1               5


<210> 38
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<400> 38

Cys Asp Cys Arg Gly Asp Cys Phe Cys
1               5


<210> 39
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<400> 39

Cys Gly Ser Leu Val Arg Cys
1               5


<210> 40
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Asp Leu Xaa Xaa Leu

1                    5

<210> 41
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Arg Thr Asp Leu Asp Ser Leu Arg Thr Tyr Thr Leu
1                    5                    10


<210> 42
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<400> 42

Arg Thr Asp Leu Asp Ser Leu Arg Thr Tyr
1                    5                    10


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<400> 43

Arg Thr Asp Leu Asp Ser Leu Arg Thr
1                    5


<210> 44
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<400> 44

Arg Thr Asp Leu Asp Ser Leu Arg
1                    5


<210> 45
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<400> 45

Gly Asp Leu Asp Leu Leu Lys Leu Arg Leu Thr Leu
1               5                   10


<210>   46
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<220>
<223>   Integrin antagonist peptide

<400>   46

Gly Asp Leu His Ser Leu Arg Gln Leu Leu Ser Arg
1               5                   10


<210>   47
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<220>
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<400>   47

Arg Asp Asp Leu His Met Leu Arg Leu Gln Leu Trp
1               5                   10


<210>   48
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Ser Ser Asp Leu His Ala Leu Lys Lys Arg Tyr Gly
1               5                   10


<210>   49
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Arg Gly Asp Leu Lys Gln Leu Ser Glu Leu Thr Trp
1               5                   10


<210>   50
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<400>  50

Cys Xaa Xaa Arg Gly Asp Cys
1               5


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Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Gly Val Ser
1               5                   10                  15


Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
            20              25


<210>  52
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<223>  Integrin antagonist peptide

<400>  52

Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Arg Val Ser
1               5                   10                  15


Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
            20              25


<210>  53
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<400>  53

Ser Arg Gly Val Asn Phe Ser Glu Trp Leu Tyr Asp Met Ser Ala Ala
1               5                   10                  15


Met Lys Glu Ala Ser Asn Val Phe Pro Ser Arg Arg Ser Arg
            20              25                  30


<210>  54
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<400>  54

Ser Ser Gln Asn Trp Asp Met Glu Ala Gly Val Glu Asp Leu Thr Ala
1               5                   10                  15

Ala Met Leu Gly Leu Leu Ser Thr Ile His Ser Ser Ser Arg
            20                  25                  30


<210>  55
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<220>
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<400>  55

Ser Ser Pro Ser Leu Tyr Thr Gln Phe Leu Val Asn Tyr Glu Ser Ala
1               5                   10                  15

Ala Thr Arg Ile Gln Asp Leu Leu Ile Ala Ser Arg Pro Ser Arg
            20                  25                  30


<210>  56
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<220>
<223>  Integrin antagonist peptide

<400>  56

Ser Ser Thr Gly Trp Val Asp Leu Leu Gly Ala Leu Gln Arg Ala Ala
1               5                   10                  15

Asp Ala Thr Arg Thr Ser Ile Pro Pro Ser Leu Gln Asn Ser Arg
            20                  25                  30


<210>  57
<211>  18
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<220>
<223>  Integrin antagonist peptide

<400>  57

Asp Val Tyr Thr Lys Lys Glu Leu Ile Glu Cys Ala Arg Arg Val Ser
1               5                   10                  15

Glu Lys
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<210> 58
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<221> misc_feature
<222> (5)..(5)
<223> Xaa is any amino acid residue

<400> 58

Arg Gly Asp Gly Xaa
1               5


<210> 59
<211> 7
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<222> (6)..(6)
<223> Xaa is any amino acid residue

<400> 59

Cys Arg Gly Asp Gly Xaa Cys
1               5


<210> 60
<211> 9
<212> PRT
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<400> 60

Cys Ala Arg Arg Leu Asp Ala Pro Cys
1               5


<210> 61
<211> 9
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<220>
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<400> 61

Cys Pro Ser Arg Leu Asp Ser Pro Cys

1                    5

<210> 62
<211> 9
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<400> 62

Cys Asp Cys Arg Gly Asp Cys Phe Cys
1                5


<210> 63
<211> 9
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<400> 63

Cys Asp Cys Arg Gly Asp Cys Leu Cys
1                5


<210> 64
<211> 12
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<400> 64

Arg Gly Asp Leu Ala Ala Leu Ser Ala Pro Pro Val
1                5                10


<210> 65
<211> 12
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<400> 65

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1                5                10


<210> 66
<211> 12
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<220>
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<400> 66

Asp Ile Thr Trp Asp Glu Leu Trp Lys Ile Met Asn
1               5                   10


<210> 67
<211> 12
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<220>
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<400> 67

Asp Tyr Thr Trp Phe Glu Leu Trp Asp Met Met Gln
1               5                   10


<210> 68
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<400> 68

Gln Ile Thr Trp Ala Gln Leu Trp Asn Met Met Lys
1               5                   10


<210> 69
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<400> 69

Asp Met Thr Trp His Asp Leu Trp Thr Leu Met Ser
1               5                   10


<210> 70
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<400> 70

Asp Tyr Ser Trp His Asp Leu Trp Glu Met Met Ser
1               5                   10


<210> 71
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<400> 71

Glu Ile Thr Trp Asp Gln Leu Trp Glu Val Met Asn
1               5               10


<210> 72
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<220>
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<400> 72

His Val Ser Trp Glu Gln Leu Trp Asp Ile Met Asn
1               5               10


<210> 73
<211> 12
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<220>
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<400> 73

His Ile Thr Trp Asp Gln Leu Trp Arg Ile Met Thr
1               5               10


<210> 74
<211> 13
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<400> 74

Arg Asn Met Ser Trp Leu Glu Leu Trp Glu His Met Lys
1               5               10


<210> 75
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<212> PRT
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<400> 75

Ala Glu Trp Thr Trp Asp Gln Leu Trp His Val Met Asn Pro Ala Glu
1               5               10                  15


Ser Gln


<210> 76

<211> 14
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<220>
<223> Selectin antagonist peptide

<400> 76

His Arg Ala Glu Trp Leu Ala Leu Trp Glu Gln Met Ser Pro
1               5                   10


<210> 77
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 77

Lys Lys Glu Asp Trp Leu Ala Leu Trp Arg Ile Met Ser Val
1               5                   10


<210> 78
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 78

Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1               5               10


<210> 79
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 79

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1               5               10


<210> 80
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 80

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1               5               10

<210> 81
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 81

Asp Ile Thr Trp Asp Gln Leu Trp Asp Leu Met Lys
1               5                   10


<210> 82
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 82

Cys Gln Asn Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Asn Glu
1               5                   10                  15


<210> 83
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 83

Ala Glu Asn Trp Ala Asp Asn Glu Pro Asn Asn Lys Arg Asn Asn Glu
1               5                   10                  15

Asp


<210> 84
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Selectin antagonist peptide

<400> 84

Arg Lys Asn Asn Lys Thr Trp Thr Trp Val Gly Thr Lys Lys Ala Leu
1               5                   10                  15

Thr Asn Glu


<210> 85
<211> 13
<212> PRT

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<213>  Artificial Sequence

<220>
<223>  Selectin antagonist peptide

<400>  85

Lys Lys Ala Leu Thr Asn Glu Ala Glu Asn Trp Ala Asp
1               5                   10


<210>  86
<211>  16
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Selectin antagonist peptide


<220>
<221>  misc_feature
<222>  (3 and)..(15)
<223>  Xaa is any amino acid residue

<400>  86

Cys Gln Xaa Arg Tyr Thr Asp Leu Val Ala Ile Gln Asn Lys Xaa Glu
1               5                   10                  15


<210>  87
<211>  17
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Selectin antagonist peptide


<220>
<221>  misc_feature
<222>  (13 and)..(15)
<223>  Xaa is any amino acid residue

<400>  87

Ala Glu Asn Trp Ala Asp Gly Glu Pro Asn Asn Lys Xaa Asn Xaa Glu
1               5                   10                  15

Asp


<210>  88
<211>  30
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Vinculin binding peptide

<400>  88

Ser Ser Gln Asn Trp Asp Met Glu Ala Gly Val Glu Asp Leu Thr Ala
1               5                   10                  15
```

Ala Met Leu Gly Leu Leu Ser Thr Ile His Ser Ser Ser Arg
            20                25                    30

<210> 89
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 89

Ser Ser Pro Ser Leu Tyr Thr Gln Phe Leu Val Asn Tyr Glu Ser Ala
1               5                   10                  15

Ala Thr Arg Ile Gln Asp Leu Leu Ile Ala Ser Arg Pro Ser Arg
            20                25                    30

<210> 90
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 90

Ser Ser Thr Gly Trp Val Asp Leu Leu Gly Ala Leu Gln Arg Ala Ala
1               5                   10                  15

Asp Ala Thr Arg Thr Ser Ile Pro Pro Ser Leu Gln Asn Ser Arg
            20                25                    30

<210> 91
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 91

Asp Val Tyr Thr Lys Lys Glu Leu Ile Glu Cys Ala Arg Arg Val Ser
1               5                   10                  15

Glu Lys

<210> 92
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 92

```
Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Gly Val Ser
1               5                   10              15
```

```
Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
            20              25
```

<210> 93
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 93

```
Ser Thr Gly Gly Phe Asp Asp Val Tyr Asp Trp Ala Arg Arg Val Ser
1               5                   10              15
```

```
Ser Ala Leu Thr Thr Thr Leu Val Ala Thr Arg
            20              25
```

<210> 94
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Vinculin binding peptide

<400> 94

```
Ser Arg Gly Val Asn Phe Ser Glu Trp Leu Tyr Asp Met Ser Ala Ala
1               5                   10              15
```

```
Met Lys Glu Ala Ser Asn Val Phe Pro Ser Arg Arg Ser Arg
            20                  25              30
```

<210> 95
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 95

```
Arg Glu Asp Val Glu Ile Leu Asp Val Tyr Ile Gly Ser Arg Pro Asp
1               5                   10              15
```

```
Ser Gly Arg
```

<210> 96
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 96

Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro Asp
1               5                   10                  15

Ser Gly Arg


<210> 97
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 97
gggggggcata tggaatgtga atctggtcca tgctgcagaa actg                    44


<210> 98
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 98
taagttcttg aaggaaggta ccatctgtaa gagagctaga ggtg                    44


<210> 99
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 99
acgacatgga cgactactgt aacggtaaga cctgtgactg cccg                    44


<210> 100
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 100
agaaacccac acaagggtcc agctacttaa tggatccgcg gccgcccagc t            51


<210> 101
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 101
ttcaagaact tacagtttct gcag                                    24


<210> 102
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 102
cgtccatgtc gtcacctcta gctc                                    24


<210> 103
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Used to form echistatin template for PCR

<400> 103
gtgtgggttt ctcgggcagt caca                                    24


<210> 104
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 104
ccgggtaaag gtggaggtgg tggtgaatgt gaatctggtc catgctgc          48


<210> 105
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 105
ccgggtaaag gtggaggtgg tggtgaatgt gaatctggtc catgctgc          48


<210> 106
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 106
aacataagta cctgtaggat cg                                      22


<210> 107
<211> 49
<212> DNA

<213> Artificial Sequence

<220>
<223> PCR primer

<400> 107
gcagcatgga ccagattcac attcaccacc acctccacct ttacccgga                49


<210> 108
<211> 859
<212> DNA
<213> Artificial Sequence

<220>
<223> Echistatin Fc-peptide


<220>
<221> misc_feature
<222> (1)..(1)
<223> NdeI site

<220>
<221> CDS
<222> (4)..(849)

<220>
<221> misc_feature
<222> (854)..(854)
<223> BamHI site

<400> 108
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cat atg gac aaa act cac aca tgt cca cct tgt cca gct ccg gaa ctc     48
    Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
    1               5                  10                  15

ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc     96
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                 20                  25                  30

ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg    144
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
             35                  40                  45

agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg    192
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
         50                  55                  60

gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc    240
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    65                  70                  75

acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg    288
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
80                  85                  90                  95

aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc    336
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                100                 105                 110

ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca    384
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            115                 120                 125

cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag    432
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        130                 135                 140
```

```
gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc    480
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    145             150             155

gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg    528
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
160             165             170             175

cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc    576
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
            180             185             190

acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc    624
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            195             200             205

gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc    672
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
    210             215             220

ctg tct ccg ggt aaa ggt gga ggt ggt ggt gaa tgt gaa tct ggt cca    720
Leu Ser Pro Gly Lys Gly Gly Gly Gly Gly Glu Cys Glu Ser Gly Pro
    225             230             235

tgc tgc aga aac tgt aag ttc ttg aag gaa ggt acc atc tgt aag aga    768
Cys Cys Arg Asn Cys Lys Phe Leu Lys Glu Gly Thr Ile Cys Lys Arg
240             245             250             255

gct aga ggt gac gac atg gac gac tac tgt aac ggt aag acc tgt gac    816
Ala Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp
            260             265             270

tgc ccg aga aac cca cac aag ggt cca gct act taatggatcc            859
Cys Pro Arg Asn Pro His Lys Gly Pro Ala Thr
            275             280
```

<210> 109
<211> 282
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 109

```
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5               10              15


Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20              25              30


Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35              40              45


His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50              55              60


Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65              70              75              80
```

```
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85              90              95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100             105             110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            115             120             125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130             135             140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145             150             155             160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
            165             170             175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180             185             190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
            195             200             205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210             215             220

Ser Pro Gly Lys Gly Gly Gly Gly Glu Cys Glu Ser Gly Pro Cys
225             230             235             240

Cys Arg Asn Cys Lys Phe Leu Lys Glu Gly Thr Ile Cys Lys Arg Ala
            245             250             255

Arg Gly Asp Asp Met Asp Asp Tyr Cys Asn Gly Lys Thr Cys Asp Cys
            260             265             270

Pro Arg Asn Pro His Lys Gly Pro Ala Thr
        275             280
```

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<210>    110
<211>    140
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    pAMG21


<220>
<221>    misc_feature
<222>    (1)..(1)
<223>    AatII site

<220>
<221>    misc_feature
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<222>  (140)..(140)
<223>  ClaI site

<400>  110
ctaattccgc tctcacctac caaacaatgc ccccctgcaa aaaataaatt cataaaaaaa      60

catacagata accatctgcg gtgataaatt atctctggcg gtgttgacat aaataccact     120

ggcggtgata ctgagcacat                                                 140


<210>  111
<211>  55
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pAMG21


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  ClaI site

<220>
<221>  misc_feature
<222>  (55)..(55)
<223>  KpnI site

<400>  111
cgatttgatt ctagaaggag gaataacata tggttaacgc gttggaattc ggtac           55


<210>  112
<211>  1546
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  pAMG21


<220>
<221>  misc_feature
<222>  (1)..(1)
<223>  AatII sticky end

<220>
<221>  misc_feature
<222>  (1546)..(1546)
<223>  SacII sticky end

<400>  112
gcgtaacgta tgcatggtct ccccatgcga gagtagggaa ctgccaggca tcaaataaaa      60

cgaaaggctc agtcgaaaga ctgggccttt cgttttatct gttgtttgtc ggtgaacgct     120

ctcctgagta ggacaaatcc gccgggagcg gatttgaacg ttgcgaagca acggcccgga     180

gggtggcggg caggacgccc gccataaact gccaggcatc aaattaagca gaaggccatc     240

ctgacggatg gcctttttgc gtttctacaa actcttttgt ttattttтct aaatacattc     300

aaatatggac gtcgtactta acttttaaag tatgggcaat caattgctcc tgttaaaatt     360

gctttagaaa tactttggca gcggtttgtt gtattgagtt tcatttgcgc attggttaaa     420
```

```
tggaaagtga ccgtgcgctt actacagcct aatattttg aaatatccca agagctttt      480

ccttcgcatg cccacgctaa acattctttt tctcttttgg ttaaatcgtt gtttgattta     540

ttatttgcta tatttatttt tcgataatta tcaactagag aaggaacaat taatggtatg     600

ttcatacacg catgtaaaaa taaactatct atatagttgt ctttctctga atgtgcaaaa     660

ctaagcattc cgaagccatt attagcagta tgaataggga aactaaaccc agtgataaga     720

cctgatgatt tcgcttcttt aattacattt ggagatttt tatttacagc attgttttca      780

aatatattcc aattaatcgg tgaatgattg gagttagaat aatctactat aggatcatat     840

tttattaaat tagcgtcatc ataatattgc ctccatttt tagggtaatt atccagaatt      900

gaaatatcag atttaaccat agaatgagga taaatgatcg cgagtaaata atattcacaa     960

tgtaccattt tagtcatatc agataagcat tgattaatat cattattgct tctacaggct    1020

ttaattttat taattattct gtaagtgtcg tcggcattta tgtctttcat acccatctct    1080

ttatccttac ctattgtttg tcgcaagttt tgcgtgttat atatcattaa aacggtaata    1140

gattgacatt tgattctaat aaattggatt tttgtcacac tattatatcg cttgaaatac    1200

aattgtttaa cataagtacc tgtaggatcg tacaggttta cgcaagaaaa tggtttgtta    1260

tagtcgatta atcgatttga ttctagattt gttttaacta attaaaggag gaataacata    1320

tggttaacgc gttggaattc gagctcacta gtgtcgacct gcagggtacc atggaagctt    1380

actcgaggat ccgcggaaag aagaagaaga agaagaaagc ccgaaaggaa gctgagttgg    1440

ctgctgccac cgctgagcaa taactagcat aaccccttgg ggcctctaaa cgggtcttga    1500

ggggtttttt gctgaaagga ggaaccgctc ttcacgctct tcacgc                   1546
```

<210> 113
<211> 872
<212> DNA
<213> Artificial Sequence

<220>
<223> GM221

<400> 113
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ttattttcgt gcggccgcac cattatcacc gccagaggta aactagtcaa cacgcacggt      60

gttagatatt tatcccttgc ggtgatagat tgagcacatc gatttgattc tagaaggagg     120

gataatatat gagcacaaaa aagaaaccat taacacaaga gcagcttgag gacgcacgtc     180

gccttaaagc aatttatgaa aaaagaaaa atgaacttgg cttatcccag gaatctgtcg      240

cagacaagat ggggatgggg cagtcaggcg ttggtgcttt atttaatggc atcaatgcat     300

taaatgctta taacgccgca ttgcttacaa aaattctcaa agttagcgtt gaagaattta     360

gcccttcaat cgccagagaa tctacgagat gtatgaagcg gttagtatgc agccgtcact     420

tagaagtgag tatgagtacc ctgttttttc tcatgttcag gcagggatgt tctcacctaa     480

gcttagaacc tttaccaaag gtgatgcgga gagatgggta agcacaacca aaaaagccag     540

tgattctgca ttctggcttg aggttgaagg taattccatg accgcaccaa caggctccaa     600
```

```
gccaagcttt cctgacggaa tgttaattct cgttgaccct gagcaggctg ttgagccagg    660

tgatttctgc atagccagac ttgggggtga tgagtttacc ttcaagaaac tgatcaggga    720

tagcggtcag gtgtttttac aaccactaaa cccacagtac ccaatgatcc catgcaatga    780

gagttgttcc gttgtgggga aagttatcgc tagtcagtgg cctgaagaga cgtttggctg    840

atagactagt ggatccacta gtgtttctgc cc                                  872
```

```
<210>    114
<211>    1197
<212>    DNA
<213>    Artificial Sequence

<220>
<223>    GM221

<400>    114
ggcggaaacc gacgtccatc gaatggtgca aaacctttcg cggtatggca tgatagcgcc     60

cggaagagag tcaattcagg gtggtgaatg tgaaaccagt aacgttatac gatgtcgcag    120

agtatgccgg tgtctcttat cagaccgttt cccgcgtggt gaaccaggcc agccacgttt    180

ctgcgaaaac gcgggaaaaa gtcgaagcgg cgatggcgga gctgaattac attcccaacc    240

gcgtggcaca caactggcg ggcaaacagt cgctcctgat tggcgttgcc acctccagtc     300

tggccctgca cgcgccgtcg caaattgtcg cggcgattaa atctcgcgcc gatcaactgg    360

gtgccagcgt ggtggtgtcg atggtagaac gaagcggcgt cgaagcctgt aaagcggcgg    420

tgcacaatct tctcgcgcaa cgcgtcagtg ggctgatcat taactatccg ctggatgacc    480

aggatgccat tgctgtggaa gctgcctgca ctaatgttcc ggcgttattt cttgatgtct    540

ctgaccagac acccatcaac agtattattt tctcccatga agacggtacg cgactgggcg    600

tggagcatct ggtcgcattg ggtcaccagc aaatcgcgct gttagcgggc ccattaagtt    660

ctgtctcggc gcgtctgcgt ctggctggct ggcataaata tctcactcgc aatcaaattc    720

agccgatagc ggaacgggaa ggcgactgga gtgccatgtc cggttttcaa caaaccatgc    780

aaatgctgaa tgagggcatc gttcccactg cgatgctggt tgccaacgat cagatggcgc    840

tgggcgcaat gcgcgccatt accgagtccg gctgcgcgt tggtgcggat atctcggtag    900

tgggatacga cgataccgaa gacagctcat gttatatccc gccgttaacc accatcaaac    960

aggattttcg cctgctgggg caaaccagcg tggaccgctt gctgcaactc tctcagggcc    1020

aggcggtgaa gggcaatcag ctgttgcccg tctcactggt gaaaagaaaa accaccctgg    1080

cgcccaatac gcaaaccgcc tctccccgcg cgttggccga ttcattaatg cagctggcac    1140

gacaggtttc ccgactggaa agcggacagt aaggtaccat aggatccagg cacagga      1197
```

```
<210>    115
<211>    11
<212>    PRT
<213>    Artificial Sequence

<220>
<223>    Laminin related peptide
```

<400> 115

Met Tyr Ile Gly Ser Arg Gly Gly Gly Gly
1               5               10


<210> 116
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 116

Met Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
1               5               10               15


<210> 117
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 117

Met Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
1               5               10               15


Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
            20               25


<210> 118
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 118

Met Ile Pro Cys Asn Asn Lys Gly Ala His Ser Val Gly Leu Met Trp
1               5               10               15


Trp Met Leu Ala Arg Gly Gly Gly Gly Gly
            20               25


<210> 119
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Laminin related peptide

<400> 119

Met Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro

1               5               10               15

Asp Ser Gly Arg Gly Gly Gly Gly Gly
            20              25

<210>   120
<211>   20
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   Laminin related peptide

<400>   120

Met Arg Gly Asp Arg Gly Asp Tyr Ile Gly Ser Arg Arg Gly Asp Gly
1               5               10               15

Gly Gly Gly Gly
            20

<210>   121
<211>   48
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Encoding Laminin related peptide, for PCR reaction to yield
        in-frame fusion to FC

<400>   121
gaataacata tgtacatcgg ttctcgtggt ggaggcggtg gggacaaa                  48

<210>   122
<211>   81
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Encoding Laminin related peptide, for PCR reaction to yield
        in-frame fusion to FC

<400>   122
gaataacata tgtacatcgg ttctcgttat attggctccc gctacattgg tagccgtgac    60

aaaactcaca catgtccacc t                                              81

<210>   123
<211>   111
<212>   DNA
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<220>
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        in-frame fusion to FC

<400>   123
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atcggctctc gctatattgg tagccgcgac aaaactcaca catgtccacc t            111

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<213>  Artificial Sequence

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gaataacata tgatcccgtg caacaacaaa ggtgctcact ctgttggtct gatgtggtgg      60

atgctggctc gtggtggagg cggtggggac aaa                                  93


<210>  125
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<220>
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       in-frame fusion to FC

<400>  125
gaataacata tgtacatcgg ttctcgtcgt gaagacgttg aaatcctgga cgttccggac      60

tctggtcgtg gtggaggcgg tggggacaaa                                      90


<210>  126
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ggcggtgggg acaaa                                                      75


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       in-frame fusion to FC

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gttattgctc agcggtggca                                                 20


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<400>  128
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Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
1               5                   10


<210>   129
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<400>   129

Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg
1               5                   10                  15


<210>   130
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Ile Gly Ser Arg
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Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr Ile Gly Ser Arg Tyr
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Ile Gly Ser Arg Tyr Ile Gly Ser Arg
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<210>   132
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<220>
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<400>   132

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1               5                   10                  15

Met Leu Ala Arg
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Tyr Ile Gly Ser Arg Arg Glu Asp Val Glu Ile Leu Asp Val Pro Asp
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Ser Gly Arg


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<400>  134
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Arg Gly Asp Arg Gly Asp Tyr Ile Gly Ser Arg Arg Gly Asp
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1               5                   10                  15


Ile Gly Ser Arg Tyr Ile Gly Ser Arg
            20                  25


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<400>  136
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Arg Glu Asp Val Glu Ile Leu Asp Val Tyr Ile Gly Ser Arg Pro Asp
1               5                   10                  15

Ser Gly Arg


<210> 137
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<400> 137

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1               5                   10                  15

Ser Gly Arg


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1               5


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<400>   140

Xaa Xaa Xaa Asp Asp Xaa Xaa Xaa
1                   5


<210>   141
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1               5                   10


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1               5


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1               5                   10


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